FIG. 1A

```
Met Leu Ala Arg Ala Leu Leu Leu Cys Ala Val Leu Ala Leu Ser His
1               5                  10                  15

Thr Ala Asn Pro Cys Cys Ser His Pro Cys Gln Asn Arg Gly Val Cys
            20                  25                  30

Met Ser Val Gly Phe Asp Gln Tyr Lys Cys Asp Cys Thr Arg Thr Gly
        35                  40                  45

Phe Tyr Gly Glu Asn Cys Ser Thr Pro Glu Phe Leu Thr Arg Ile Lys
    50                  55                  60

Leu Phe Leu Lys Pro Thr Pro Asn Thr Val His Tyr Ile Leu Thr His
65                  70                  75                  80

Phe Lys Gly Phe Trp Asn Val Val Asn Asn Ile Pro Phe Leu Arg Asn
                85                  90                  95

Ala Ile Met Ser Tyr Val Leu Thr Ser Arg Ser His Leu Ile Asp Ser
            100                 105                 110

Pro Pro Thr Tyr Asn Ala Asp Tyr Gly Tyr Lys Ser Trp Glu Ala Phe
        115                 120                 125

Ser Asn Leu Ser Tyr Tyr Thr Arg Ala Leu Pro Pro Val Pro Asp Asp
    130                 135                 140

Cys Pro Thr Pro Leu Gly Val Lys Gly Lys Lys Gln Leu Pro Asp Ser
145                 150                 155                 160

Asn Glu Ile Val Glu Lys Leu Leu Leu Arg Arg Lys Phe Ile Pro Asp
                165                 170                 175

Pro Gln Gly Ser Asn Met Met Phe Ala Phe Phe Ala Gln His Phe Thr
            180                 185                 190

His Gln Phe Phe Lys Thr Asp His Lys Arg Gly Pro Ala Phe Thr Asn
        195                 200                 205

Gly Leu Gly His Gly Val Asp Leu Asn His Ile Tyr Gly Glu Thr Leu
    210                 215                 220

Ala Arg Gln Arg Lys Leu Arg Leu Phe Lys Asp Gly Lys Met Lys Tyr
225                 230                 235                 240

Gln Ile Ile Asp Gly Glu Met Tyr Pro Pro Thr Val Lys Asp Thr Gln
                245                 250                 255

Ala Glu Met Ile Tyr Pro Pro Gln Val Pro Glu His Leu Arg Phe Ala
            260                 265                 270

Val Gly Gln Glu Val Phe Gly Leu Val Pro Gly Leu Met Met Tyr Ala
        275                 280                 285

Thr Ile Trp Leu Arg Glu His Asn Arg Val Cys Asp Val Leu Lys Gln
    290                 295                 300
```

FIG. 1B

```
Glu His Pro Glu Trp Gly Asp Glu Gln Leu Phe Gln Thr Ser Arg Leu
305                 310                 315                 320

Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu Asp Tyr Val Gln
                325                 330                 335

His Leu Ser Gly Tyr His Phe Lys Leu Lys Phe Asp Pro Glu Leu Leu
            340                 345                 350

Phe Asn Lys Gln Phe Gln Tyr Gln Asn Arg Ile Ala Ala Glu Phe Asn
        355                 360                 365

Thr Leu Tyr His Trp His Pro Leu Leu Pro Asp Thr Phe Gln Ile His
    370                 375                 380

Asp Gln Lys Tyr Asn Tyr Gln Gln Phe Ile Tyr Asn Asn Ser Ile Leu
385                 390                 395                 400

Leu Glu His Gly Ile Thr Gln Phe Val Glu Ser Phe Thr Arg Gln Ile
                405                 410                 415

Ala Gly Arg Val Ala Gly Gly Arg Asn Val Pro Pro Ala Val Gln Lys
            420                 425                 430

Val Ser Gln Ala Ser Ile Asp Gln Ser Arg Gln Met Lys Tyr Gln Ser
        435                 440                 445

Phe Asn Glu Tyr Arg Lys Arg Phe Met Leu Lys Pro Tyr Glu Ser Phe
    450                 455                 460

Glu Glu Leu Thr Gly Glu Lys Glu Met Ser Ala Glu Leu Glu Ala Leu
465                 470                 475                 480

Tyr Gly Asp Ile Asp Ala Val Glu Leu Tyr Pro Ala Leu Leu Val Glu
                485                 490                 495

Lys Pro Arg Pro Asp Ala Ile Phe Gly Glu Thr Met Val Glu Val Gly
            500                 505                 510

Ala Pro Phe Ser Leu Lys Gly Leu Met Gly Asn Val Ile Cys Ser Pro
        515                 520                 525

Ala Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val Gly Phe Gln Ile
    530                 535                 540

Ile Asn Thr Ala Ser Ile Gln Ser Leu Ile Cys Asn Asn Val Lys Gly
545                 550                 555                 560

Cys Pro Phe Thr Ser Phe Ser Val Pro Asp Pro Glu Leu Ile Lys Thr
                565                 570                 575

Val Thr Ile Asn Ala Ser Ser Ser Arg Ser Gly Leu Asp Asp Ile Asn
            580                 585                 590

Pro Thr Val Leu Leu Lys Glu Arg Ser Thr Glu Leu (SEQ ID NO: 10)
        595                 600
```

FIG. 2A

```
GTCCAGGAAC TCCTCAGCAG CGCCTCCTTC AGCTCCACAG CCAGACGCCC TCAGACAGCA   60
AAGCCTACCC CCGCGCCGCG CCCTGCCCGC CGCTGCGATG CTCGCCCGCG CCCTGCTGCT  120
GTGCGCGGTC CTGGCGCTCA GCCATACAGC AAATCCTTGC TGTTCCCACC CATGTCAAAA  180
CCGAGGTGTA TGTATGAGTG TGGGATTTGA CCAGTATAAG TGCGATTGTA CCCGGACAGG  240
ATTCTATGGA GAAAACTGCT CAACACCGGA ATTTTTGACA AGAATAAAAT TATTTCTGAA  300
ACCCACTCCA AACACAGTGC ACTACATACT TACCCACTTC AAGGGATTTT GGAACGTTGT  360
GAATAACATT CCCTTCCTTC GAAATGCAAT TATGAGTTAT GTGTTGACAT CCAGATCACA  420
TTTGATTGAC AGTCCACCAA CTTACAATGC TGACTATGGC TACAAAAGCT GGGAAGCCTT  480
CTCTAACCTC TCCTATTATA CTAGAGCCCT TCCTCCTGTG CCTGATGATT GCCCGACTCC  540
CTTGGGTGTC AAAGGTAAAA AGCAGCTTCC TGATTCAAAT GAGATTGTGG AAAAATTGCT  600
TCTAAGAAGA AAGTTCATCC CTGATCCCCA GGGCTCAAAC ATGATGTTTG CATTCTTTGC  660
CCAGCACTTC ACGCACCAGT TTTTCAAGAC AGATCATAAG CGAGGGCCAG CTTTCACCAA  720
CGGGCTGGGC CATGGGGTGG ACTTAAATCA TATTTACGGT GAAACTCTGG CTAGACAGCG  780
TAAACTGCGC CTTTTCAAGG ATGGAAAAAT GAAATATCAG ATAATTGATG GAGAGATGTA  840
TCCTCCCACA GTCAAAGATA CTCAGGCAGA GATGATCTAC CCTCCTCAAG TCCCTGAGCA  900
TCTACGGTTT GCTGTGGGGC AGGAGGTCTT TGGTCTGGTG CCTGGTCTGA TGATGTATGC  960
CACAATCTGG CTGCGGGAAC ACAACAGAGT ATGTGATGTG CTTAAACAGG AGCATCCTGA 1020
ATGGGGTGAT GAGCAGTTGT TCCAGACAAG CAGGCTAATA CTGATAGGAG AGACTATTAA 1080
GATTGTGATT GAAGATTATG TGCAACACTT GAGTGGCTAT CACTTCAAAC TGAAATTTGA 1140
CCCAGAACTA CTTTTCAACA AACAATTCCA GTACCAAAAT CGTATTGCTG CTGAATTTAA 1200
CACCCTCTAT CACTGGCATC CCCTTCTGCC TGACACCTTT CAAATTCATG ACCAGAAATA 1260
CAACTATCAA CAGTTTATCT ACAACAACTC TATATTGCTG GAACATGGAA TTACCCAGTT 1320
TGTTGAATCA TTCACCAGGC AAATTGCTGG CAGGGTTGCT GGTGGTAGGA ATGTTCCACC 1380
CGCAGTACAG AAAGTATCAC AGGCTTCCAT TGACCAGAGC AGGCAGATGA AATACCAGTC 1440
TTTTAATGAG TACCGCAAAC GCTTTATGCT GAAGCCCTAT GAATCATTTG AAGAACTTAC 1500
AGGAGAAAAG GAAATGTCTG CAGAGTTGGA AGCACTCTAT GGTGACATCG ATGCTGTGGA 1560
GCTGTATCCT GCCCTTCTGG TAGAAAAGCC TCGGCCAGAT GCCATCTTTG GTGAAACCAT 1620
GGTAGAAGTT GGAGCACCAT TCTCCTTGAA AGGACTTATG GGTAATGTTA TATGTTCTCC 1680
TGCCTACTGG AAGCCAAGCA CTTTTGGTGG AGAAGTGGGT TTTCAAATCA TCAACACTGC 1740
```

FIG. 2B

CTCAATTCAG TCTCTCATCT GCAATAACGT GAAGGGCTGT CCCTTTACTT CATTCAGTGT 1800
TCCAGATCCA GAGCTCATTA AAACAGTCAC CATCAATGCA AGTTCTTCCC GCTCCGGACT 1860
AGATGATATC AATCCCACAG TACTACTAAA AGAACGGTCG ACTGAACTGT AGAAGTCTAA 1920
TGATCATATT TATTTATTTA TATGAACCAT GTCTATTAAT TTAATTATTT AATAATATTT 1980
ATATTAAACT CCTTATGTTA CTTAACATCT TCTGTAACAG AAGTCAGTAC TCCTGTTGCG 2040
GAGAAAGGAG TCATACTTGT GAAGACTTTT ATGTCACTAC TCTAAAGATT TTGCTGTTGC 2100
TGTTAAGTTT GGAAAACAGT TTTTATTCTG TTTTATAAAC CAGAGAGAAA TGAGTTTTGA 2160
CGTCTTTTTA CTTGAATTTC AACTTATATT ATAAGGACGA AAGTAAAGAT GTTTGAATAC 2220
TTAAACACTA TCACAAGATG CCAAAATGCT GAAAGTTTTT ACACTGTCGA TGTTTCCAAT 2280
GCATCTTCCA TGATGCATTA GAAGTAACTA ATGTTTGAAA TTTTAAAGTA CTTTTGGGTA 2340
TTTTTCTGTC ATCAAACAAA ACAGGTATCA GTGCATTATT AAATGAATAT TTAAATTAGA 2400
CATTACCAGT AATTTCATGT CTACTTTTTA AAATCAGCAA TGAAACAATA ATTTGAAATT 2460
TCTAAATTCA TAGGGTAGAA TCACCTGTAA AAGCTTGTTT GATTTCTTAA AGTTATTAAA 2520
CTTGTACATA TACCAAAAAG AAGCTGTCTT GGATTTAAAT CTGTAAAATC AGATGAAATT 2580
TTACTACAAT TGCTTGTTAA AATATTTTAT AAGTGATGTT CCTTTTTCAC CAAGAGTATA 2640
AACCTTTTTA GTGTGACTGT TAAAACTTCC TTTTAAATCA AAATGCCAAA TTTATTAAGG 2700
TGGTGGAGCC ACTGCAGTGT TATCTCAAAA TAAGAATATC CTGTTGAGAT ATTCCAGAAT 2760
CTGTTTATAT GGCTGGTAAC ATGTAAAAAC CCCATAACCC CGCCAAAAGG GGTCCTACCC 2820
TTGAACATAA AGCAATAACC AAAGGAGAAA AGCCCAAATT ATTGGTTCCA AATTTAGGGT 2880
TTAAACTTTT TGAAGCAAAC TTTTTTTTAG CCTTGTGCAC TGCAGACCTG GTACTCAGAT 2940
TTTGCTATGA GGTTAATGAA GTACCAAGCT GTGCTTGAAT AACGATATGT TTTCTCAGAT 3000
TTTCTGTTGT ACAGTTTAAT TTAGCAGTCC ATATCACATT GCAAAAGTAG CAATGACCTC 3060
ATAAAATACC TCTTCAAAAT GCTTAAATTC ATTTCACACA TTAATTTTAT CTCAGTCTTG 3120
AAGCCAATTC AGTAGGTGCA TTGGAATCAA GCCTGGCTAC CTGCATGCTG TTCCTTTTCT 3180
TTTCTTCTTT TAGCCATTTT GCTAAGAGAC ACAGTCTTCT CAAACACTTC GTTTCTCCTA 3240
TTTTGTTTTA CTAGTTTTAA GATCAGAGTT CACTTTCTTT GGACTCTGCC TATATTTTCT 3300
TACCTGAACT TTTGCAAGTT TTCAGGTAAA CCTCAGCTCA GGACTGCTAT TTAGCTCCTC 3360
TTAAGAAGAT TAAAAAAAAA AAAAAAG (SEQ ID NO: 11) 3387

Annotated Sheets Showing Changes

FIG. 1A

```
Met Leu Ala Arg Ala Leu Leu Leu Cys Ala Val Leu Ala Leu Ser His
1               5                  10                  15

Thr Ala Asn Pro Cys Cys Ser His Pro Cys Gln Asn Arg Gly Val Cys
            20                  25                  30

Met Ser Val Gly Phe Asp Gln Tyr Lys Cys Asp Cys Thr Arg Thr Gly
        35                  40                  45

Phe Tyr Gly Glu Asn Cys Ser Thr Pro Glu Phe Leu Thr Arg Ile Lys
    50                  55                  60

Leu Phe Leu Lys Pro Thr Pro Asn Thr Val His Tyr Ile Leu Thr His
65                  70                  75                  80

Phe Lys Gly Phe Trp Asn Val Val Asn Asn Ile Pro Phe Leu Arg Asn
                85                  90  90                  95

Ala Ile Met Ser Tyr Val Leu Thr Ser Arg Ser His Leu Ile Asp Ser
            100                 105                 110

Pro Pro Thr Tyr Asn Ala Asp Tyr Gly Tyr Lys Ser Trp Glu Ala Phe
        115                 120                 125

Ser Asn Leu Ser Tyr Tyr Thr Arg Ala Leu Pro Pro Val Pro Asp Asp
    130                 135                 140

Cys Pro Thr Pro Leu Gly Val Lys Gly Lys Lys Gln Leu Pro Asp Ser
145                 150                 155                 160

Asn Glu Ile Val Glu Lys Leu Leu Leu Arg Arg Lys Phe Ile Pro Asp
                165                 170                 175

Pro Gln Gly Ser Asn Met Met Phe Ala Phe Phe Ala Gln His Phe Thr
            180                 185                 190

His Gln Phe Phe Lys Thr Asp His Lys Arg Gly Pro Ala Phe Thr Asn
        195                 200                 205

Gly Leu Gly His Gly Val Asp Leu Asn His Ile Tyr Gly Glu Thr Leu
    210                 215                 220

Ala Arg Gln Arg Lys Leu Arg Leu Phe Lys Asp Gly Lys Met Lys Tyr
225                 230                 235                 240

Gln Ile Ile Asp Gly Glu Met Tyr Pro Pro Thr Val Lys Asp Thr Gln
                245                 250                 255

Ala Glu Met Ile Tyr Pro Pro Gln Val Pro Glu His Leu Arg Phe Ala
            260                 265                 270

Val Gly Gln Glu Val Phe Gly Leu Val Pro Gly Leu Met Met Tyr Ala
        275                 280                 285

Thr Ile Trp Leu Arg Glu His Asn Arg Val Cys Asp Val Leu Lys Gln
    290                 295                 300
```

Annotated Sheets Showing Changes

FIG. 1B

```
Glu His Pro Glu Trp Gly Asp Glu Gln Leu Phe Gln Thr Ser Arg Leu
305                 310                 315                 320

Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu Asp Tyr Val Gln
                325                 330                 335

His Leu Ser Gly Tyr His Phe Lys Leu Lys Phe Asp Pro Glu Leu Leu
            340                 345                 350

Phe Asn Lys Gln Phe Gln Tyr Gln Asn Arg Ile Ala Ala Glu Phe Asn
        355                 360                 365

Thr Leu Tyr His Trp His Pro Leu Leu Pro Asp Thr Phe Gln Ile His
    370                 375                 380

Asp Gln Lys Tyr Asn Tyr Gln Gln Phe Ile Tyr Asn Asn Ser Ile Leu
385                 390                 395                 400

Leu Glu His Gly Ile Thr Gln Phe Val Glu Ser Phe Thr Arg Gln Ile
                405                 410                 415

Ala Gly Arg Val Ala Gly Gly Arg Asn Val Pro Pro Ala Val Gln Lys
            420                 425                 430

Val Ser Gln Ala Ser Ile Asp Gln Ser Arg Gln Met Lys Tyr Gln Ser
        435                 440                 445

Phe Asn Glu Tyr Arg Lys Arg Phe Met Leu Lys Pro Tyr Glu Ser Phe
    450                 455                 460

Glu Glu Leu Thr Gly Glu Lys Glu Met Ser Ala Glu Leu Glu Ala Leu
465                 470                 475                 480

Tyr Gly Asp Ile Asp Ala Val Glu Leu Tyr Pro Ala Leu Leu Val Glu
                485                 490                 495

Lys Pro Arg Pro Asp Ala Ile Phe Gly Glu Thr Met Val Glu Val Gly
            500                 505                 510

Ala Pro Phe Ser Leu Lys Gly Leu Met Gly Asn Val Ile Cys Ser Pro
        515                 520                 525

Ala Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val Gly Phe Gln Ile
    530                 535                 540

Ile Asn Thr Ala Ser Ile Gln Ser Leu Ile Cys Asn Asn Val Lys Gly
545                 550                 555                 560

Cys Pro Phe Thr Ser Phe Ser Val Pro Asp Pro Glu Leu Ile Lys Thr
                565                 570                 575

Val Thr Ile Asn Ala Ser Ser Ser Arg Ser Gly Leu Asp Asp Ile Asn
            580                 585                 590

Pro Thr Val Leu Leu Lys Glu Arg Ser Thr Glu Leu (SEQ ID NO: 10)
        595                 600
```

Annotated Sheets Showing Changes

FIG. 2A

GTCCAGGAAC TCCTCAGCAG CGCCTCCTTC AGCTCCACAG CCAGACGCCC TCAGACAGCA 60
AAGCCTACCC CCGCGCCGCG CCCTGCCCGC CGCTGCGATG CTCGCCCGCG CCCTGCTGCT 120
GTGCGCGGTC CTGGCGCTCA GCCATACAGC AAATCCTTGC TGTTCCCACC CATGTCAAAA 180
CCGAGGTGTA TGTATGAGTG TGGGATTTGA CCAGTATAAG TGCGATTGTA CCCGGACAGG 240
ATTCTATGGA GAAAACTGCT CAACACCGGA ATTTTTGACA AGAATAAAAT TATTTCTGAA 300
ACCCACTCCA AACACAGTGC ACTACATACT TACCCACTTC AAGGGATTTT GGAACGTTGT 360
GAATAACATT CCCTTCCTTC GAAATGCAAT TATGAGTTAT GTGTTGACAT CCAGATCACA 420
TTTGATTGAC AGTCCACCAA CTTACAATGC TGACTATGGC TACAAAAGCT GGGAAGCCTT 480
CTCTAACCTC TCCTATTATA CTAGAGCCCT TCCTCCTGTG CCTGATGATT GCCCGACTCC 540
CTTGGGTGTC AAAGGTAAAA AGCAGCTTCC TGATTCAAAT GAGATTGTGG AAAAATTGCT 600
TCTAAGAAGA AAGTTCATCC CTGATCCCCA GGGCTCAAAC ATGATGTTTG CATTCTTTGC 660
CCAGCACTTC ACGCACCAGT TTTTCAAGAC AGATCATAAG CGAGGGCCAG CTTTCACCAA 720
CGGGCTGGGC CATGGGGTGG ACTTAAATCA TATTTACGGT GAAACTCTGG CTAGACAGCG 780
TAAACTGCGC CTTTTCAAGG ATGGAAAAAT GAAATATCAG ATAATTGATG GAGAGATGTA 840
TCCTCCCACA GTCAAAGATA CTCAGGCAGA GATGATCTAC CCTCCTCAAG TCCCTGAGCA 900
TCTACGGTTT GCTGTGGGGC AGGAGGTCTT TGGTCTGGTG CCTGGTCTGA TGATGTATGC 960
CACAATCTGG CTGCGGGAAC ACAACAGAGT ATGTGATGTG CTTAAACAGG AGCATCCTGA 1020
ATGGGGTGAT GAGCAGTTGT TCCAGACAAG CAGGCTAATA CTGATAGGAG AGACTATTAA 1080
GATTGTGATT GAAGATTATG TGCAACACTT GAGTGGCTAT CACTTCAAAC TGAAATTTGA 1140
CCCAGAACTA CTTTTCAACA AACAATTCCA GTACCAAAAT CGTATTGCTG CTGAATTTAA 1200
CACCCTCTAT CACTGGCATC CCCTTCTGCC TGACACCTTT CAAATTCATG ACCAGAAATA 1260
CAACTATCAA CAGTTTATCT ACAACAACTC TATATTGCTG GAACATGGAA TTACCCAGTT 1320
TGTTGAATCA TTCACCAGGC AAATTGCTGG CAGGGTTGCT GGTGGTAGGA ATGTTCCACC 1380
CGCAGTACAG AAAGTATCAC AGGCTTCCAT TGACCAGAGC AGGCAGATGA AATACCAGTC 1440
TTTTAATGAG TACCGCAAAC GCTTTATGCT GAAGCCCTAT GAATCATTTG AAGAACTTAC 1500
AGGAGAAAAG GAAATGTCTG CAGAGTTGGA AGCACTCTAT GGTGACATCG ATGCTGTGGA 1560
GCTGTATCCT GCCCTTCTGG TAGAAAAGCC TCGGCCAGAT GCCATCTTTG GTGAAACCAT 1620
GGTAGAAGTT GGAGCACCAT TCTCCTTGAA AGGACTTATG GGTAATGTTA TATGTTCTCC 1680
TGCCTACTGG AAGCCAAGCA CTTTTGGTGG AGAAGTGGGT TTTCAAATCA TCAACACTGC 1740

Annotated Sheets Showing Changes

FIG. 2B

CTCAATTCAG TCTCTCATCT GCAATAACGT GAAGGGCTGT CCCTTTACTT CATTCAGTGT 1800
TCCAGATCCA GAGCTCATTA AAACAGTCAC CATCAATGCA AGTTCTTCCC GCTCCGGACT 1860
AGATGATATC AATCCCACAG TACTACTAAA AGAACGGTCG ACTGAACTGT AGAAGTCTAA 1920
TGATCATATT TATTTATTTA TATGAACCAT GTCTATTAAT TTAATTATTT AATAATATTT 1980
ATATTAAACT CCTTATGTTA CTTAACATCT TCTGTAACAG AAGTCAGTAC TCCTGTTGCG 2040
GAGAAAGGAG TCATACTTGT GAAGACTTTT ATGTCACTAC TCTAAAGATT TTGCTGTTGC 2100
TGTTAAGTTT GGAAAACAGT TTTTATTCTG TTTTATAAAC CAGAGAGAAA TGAGTTTTGA 2160
CGTCTTTTTA CTTGAATTTC AACTTATATT ATAAGGACGA AAGTAAAGAT GTTTGAATAC 2220
TTAAACACTA TCACAAGATG CCAAAATGCT GAAAGTTTTT ACACTGTCGA TGTTTCCAAT 2280
GCATCTTCCA TGATGCATTA GAAGTAACTA ATGTTTGAAA TTTTAAAGTA CTTTTGGGTA 2340
TTTTTCTGTC ATCAAACAAA ACAGGTATCA GTGCATTATT AAATGAATAT TTAAATTAGA 2400
CATTACCAGT AATTTCATGT CTACTTTTTA AAATCAGCAA TGAAACAATA ATTTGAAATT 2460
TCTAAATTCA TAGGGTAGAA TCACCTGTAA AAGCTTGTTT GATTTCTTAA AGTTATTAAA 2520
CTTGTACATA TACCAAAAAG AAGCTGTCTT GGATTTAAAT CTGTAAAATC AGATGAAATT 2580
TTACTACAAT TGCTTGTTAA AATATTTTAT AAGTGATGTT CCTTTTTCAC CAAGAGTATA 2640
AACCTTTTTA GTGTGACTGT TAAAACTTCC TTTTAAATCA AAATGCCAAA TTTATTAAGG 2700
TGGTGGAGCC ACTGCAGTGT TATCTCAAAA TAAGAATATC CTGTTGAGAT ATTCCAGAAT 2760
CTGTTTATAT GGCTGGTAAC ATGTAAAAAC CCCATAACCC CGCCAAAAGG GGTCCTACCC 2820
TTGAACATAA AGCAATAACC AAAGGAGAAA AGCCCAAATT ATTGGTTCCA AATTTAGGGT 2880
TTAAACTTTT TGAAGCAAAC TTTTTTTTAG CCTTGTGCAC TGCAGACCTG GTACTCAGAT 2940
TTTGCTATGA GGTTAATGAA GTACCAAGCT GTGCTTGAAT AACGATATGT TTTCTCAGAT 3000
TTTCTGTTGT ACAGTTTAAT TTAGCAGTCC ATATCACATT GCAAAAGTAG CAATGACCTC 3060
ATAAAATACC TCTTCAAAAT GCTTAAATTC ATTTCACACA TTAATTTTAT CTCAGTCTTG 3120
AAGCCAATTC AGTAGGTGCA TTGGAATCAA GCCTGGCTAC CTGCATGCTG TTCCTTTTCT 3180
TTTCTTCTTT TAGCCATTTT GCTAAGAGAC ACAGTCTTCT CAAACACTTC GTTTCTCCTA 3240
TTTTGTTTTA CTAGTTTTAA GATCAGAGTT CACTTTCTTT GGACTCTGCC TATATTTTCT 3300
TACCTGAACT TTTGCAAGTT TTCAGGTAAA CCTCAGCTCA GGACTGCTAT TTAGCTCCTC 3360
TTAAGAAGAT TAAAAAAAAA AAAAAAG (SEQ ID NO: 11) 3387